

Scoring table:	OLIGO			
GapOp:	60.0 , Gapext 60.0			
Searched:	127863 seqs, 47026705 residues			
Word size :	0			
Total number of hits satisfying chosen parameters:	127863			
Minimum DB seq length:	0			
Maximum DB seq length:	2000000000			
Post-processing:	Listing first 45 summaries			
Database :	SwissProt_41.1*			
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
<b>SUMMARIES</b>				
Result No.	Score	Query Match Length	DB ID	Description
1	7	36.8	145 1 YV40_DEIRA	09rs84 deinococcus
2	7	36.8	193 1 VC07_ADE04	Q96811 human adeno
3	7	36.8	263 1 CCMC_BRAJA	P30912 bradyrhizob
4	7	36.8	291 1 YM32_MYCTOB	Q10515 mycobacteri
5	7	36.8	326 1 Y083_CAUCR	P37835 caulobacter
6	7	36.8	362 1 CRKA_HUMAN	P46092 homo sapien
7	7	36.8	381 1 ARGJ_THETHAN	P96137 thermus the
8	7	36.8	383 1 SUC2_STRCO	087840 streptomyce
9	7	36.8	387 1 ARGJ_MICKA	Q8zjg3 m arginine
10	7	36.8	394 1 FXD3_CHICK	P79772 gallus gallu
11	7	36.8	417 1 PROA_MEIRU	086553 melothrixmus
12	7	36.8	423 1 CESS_BUTMAN	Q9bw77 homo sapien
13	7	36.8	428 1 Y486_MYCTOB	P54138 mycobacteri
14	7	36.8	444 1 VGLX_ISVBS	Q08403 bovine herp
15	7	36.8	448 1 TRME_XANAC	Q8pe19 xanthomonas
16	7	36.8	474 1 CYAE_BORPE	P11992 bordetella
17	7	36.8	480 1 Y486_MYCTOB	Q11512 mycobacteri
18	7	36.8	499 1 GSHR_PLAKF	015770 plasmocytid
19	7	36.8	499 1 GSHR_PLAKF	Q94455 plasmocytid
20	7	36.8	521 1 EX7L_RHILLO	Q984v3 rhizobium 1
21	7	36.8	603 1 OS26_HCMVIA	P09299 human cytom
22	7	36.8	621 1 HEML_AGABI	Q9203 agaricus bi
23	7	36.8	742 1 ULA4_ISVBP	P30021 bovine herp
24	7	36.8	777 1 METE_GAUCR	Q9aw11 caulobacter
25	7	36.8	799 1 SYFB_GAUCR	Q9as65 pseudorickettsia
26	7	36.8	913 1 VGLB_PRVIF	P08355 epstein-bar
27	7	36.8	1318 1 VP14_EBV	P45387 haemophilus
28	7	36.8	1394 1 HAP_HAEIN	Q15240 homo sapien
29	7	36.8	2390 1 SPCP_HUMAN	Q96651 homo sapien
30	7	36.8	4523 1 DYHB_HUMAN	Q91399 neisseria m
31	6	31.6	68 1 RPOZ_NEIMA	Q06124 bacterioph
32	6	31.6	74 1 Y082_BPP2	P43740 haemophilus
33	6	31.6	88 1 RPOZ_HAEIN	



Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Holt R.J., Kolenow J.F., Nelson W.C., Omayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.; "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains." Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

-1- SIMILARITY: BELONGS TO THE CBPY/CBZ/GPH/YIEH FAMILY.

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CC DR EMBL; M91449; AAA23053.1; -.

CC DR EMBL; AE005917; AAK24454.1; -.

CC DR PIR; B87557; B7557.

CC DR PIR; S27534; S27534.

CC DR TIGR; CC2483; -.

CC DR InterPro; IPR03593; AAA\_ATPase.

CC DR InterPro; IPRO05129; ArgK.

CC DR Pfam; PF03308; ArgK; 1.

CC DR SMART; SM00302; AAA; 1.

CC DR TIGRFAMS; TIGR00750; Iao; 1.

CC KW Hypothetical protein; ATP-binding; Complete proteome.

CC FT NP\_BIND 61 68 ATP (POTENTIAL).

CC FT CONFLICT 77 77 N->K (IN REF. 1).

CC SQ SEQUENCE 326 AA; 34550 MW; 3F58763201CEF32D CRC64;

Query Match 36.8%; Score 7; DB 1; Length 326; Best Local Similarity 100.0%; Prod. No. 19; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARARRA 7

Db 264 ARARRA 270

RESULT 6

CKRA\_HUMAN STANDARD; PRT; 362 AA.

ID CKRA\_HUMAN STANDARD; PRT; 362 AA.

AC PA6092; Q9NZG2;

DT 01-NOV-1995 (Rel. 32, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE C-C chemokine receptor type 10 (C-C CKR-10) (CCR-10) (G-CPBP2 OR CCR10).

GN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OC NCBI\_TAXID=9606;

OX [1]

RN RP SEQUENCE FROM N.A., AND CHARACTERIZATION.

RX MEDLINE=20191997; PubMed=10725636;

RA RA Clark-Lewis I., Gerard C.,

RA RA Jamison D.I., Rits M., Bota D., Gerard N.P., Graham G.J., Lehmann P., Oldham E., Zlotnik A.,

RA RA J. Immunol. 164:3460-3464 (2000).

RN [2]

RP SEQUENCE FROM N.A., AND CHARACTERIZATION.

RX MEDLINE=20191998; PubMed=10725697;

RA RA Honey B., Wang W., Soto H., Buchanan M.E., Wiesenborn A., Catron D., Muller A., McClaughan T.K., Dieu Nost Jean M.C., Orozco R., Ruzicka T.,

RA RA Lehnmann P., Oldham E., Zlotnik A.,

RT RT "The orphan chemokine receptor G protein-coupled receptor 2 (GPR-2, CCR10) binds the skin-associated chemokine CCL27 (Crank/ALP/ILC)." J. Immunol. 164:3465-3470 (2000).

RN [3]

RP SEQUENCE OF 9-362 FROM N.A.

RX MEDLINE=9515831; PubMed=7651889;

RA RA Marchese A., Docherty J.M., Nguyen T., Heiber M., Cheng R., Heng H.H.Q., Tsui L.-C., Shi X., George O'Dowd B.F., Hwang H.H.Q., "Cloning of human genes encoding novel G protein-coupled receptors." Genomics 23:609-618 (1994).

RN [4]

RP LIGAND BINDING, AND TISSUE SPECIFICITY.

RX MEDLINE=20357357; PubMed=10781587;

Wang W., Soto H., Oldham E.R., Buchanan M.E., Honey B., Catron D., Jenkins N., Copeland N.G., Gilbert D.J., Nguyen N., Abrams J., Kershnarovich D., Smith K., McClanahan T., Vicari A.P., Zlotnik A.; "Identification of a novel chemokine (CCl28), which binds CCR10 (GPR2);"; J. Biol. Chem. 275:22313-22323 (2000).  
 [5]

RP LIGAND BINDING.  
 RX MEDLINE=20432268; PubMed=10975800;  
 RA Pan J., Kunkel E.J., Gossler U., Lazarus N., Langdon P., Broadwell K., Vieria M.A., Genovese M.C., Butcher E.C., Soler D.;  
 RT "A novel chemokine ligand for CCR10 and CCR3 expressed by epithelial cells in mucosal tissues";  
 RL J. Immunol. 165:2943-2949 (2000).  
 -1- FUNCTION: RECEPTOR FOR CHEMOKINES SCYA27 AND SCYA28. SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL AND STIMULATES CHEMOTAXIS IN A PRE-B CELL LINE.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN ADULT TESTIS, SMALL INTESTINE, FETAL LONG FETAL KIDNEY. WEAKER EXPRESSION WAS OBSERVED IN MANY OTHER ADULT TISSUES INCLUDING SPLEEN, THYMUS, LYMPH NODE, PEYER'S PATCHES, COLON, HEART, Ovary, PERIPHERAL BLOOD LYMPHOCYTES, THYROID AND SPINAL CORD. ALSO EXPRESSED BY MELANOCYTES, DERMAL FIBROBLASTS, DERMAL MICROVASCULAR ENDOTHELIAL CELLS. ALSO DETECTED IN T CELLS AND IN SKIN-DERIVED LANGERHANS CELLS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC EMBL; AF215981; AAIF6709\_1.; DR GO:0005887; C: Integral to plasma membrane; TAS.  
 DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . . ; TAS.  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR Pfam; PF00001; 7tm\_1.; DR PRINTS; PR001557; CHEMOKINGER10.  
 DR PROSITE; PS00237; G\_PROTEIN\_PRCEP\_F1\_1.; DR PROSITE; PS00237; G\_PROTEIN\_PRCEP\_F1\_2.; DR DOMAIN 1 52 G-protein coupled receptor, transmembrane, glycoprotein.  
 FT DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 53 68 1 (POTENTIAL).  
 FT DOMAIN 69 78 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 79 99 2 (POTENTIAL).  
 FT DOMAIN 100 114 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 115 136 3 (POTENTIAL).  
 FT DOMAIN 137 159 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 160 179 4 (POTENTIAL).  
 FT DOMAIN 180 203 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 204 225 5 (POTENTIAL).  
 FT DOMAIN 226 247 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 248 269 6 (POTENTIAL).  
 FT DOMAIN 270 290 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 291 313 7 (POTENTIAL).  
 FT DOMAIN 314 362 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 113 191 BY SIMILARITY.  
 FT CONFLICT 51 51 V->L (IN REF. 3).  
 FT CONFLICT 235 235 MISSING (IN REF. 2).  
 FT CONFLICT 330 330 S->C (IN REF. 2).  
 SEQUENCE 362 AA; 38399 MW; 69DF12B639AEE99A CRC64;

Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ARRRAA9 11111  
 Db 68 ARRRAA9 74

RESULT 7  
 ARGJ\_7THETH STANDARD; PRT; 381 AA.  
 ID ARGJ\_7THETH  
 AC P96137;  
 DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Glutamate N-Acetyltransferase (EC 2.3.1.35) (Ornithine acetyltransferase) (Ornithine transacetylase) (Oxtrase) [Contains: DE Glutamate N-Acetyltransferase alpha chain; Glutamate N- DE acetyltransferase beta chain].  
 ARGJ.  
 OS Thermus thermophilus.  
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae; Thermus.  
 OC OR  
 RN [1] N.A.  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HB27;  
 RX MEDLINE=98154436; PubMed=9493385;  
 RA Baetens M., Legrain C., Boyen A.; Glansdorff N.;  
 RT Genes and enzymes of the acetyl cycle of arginine biosynthesis in the extreme thermophilic bacterium *Thermus thermophilus* HB27.;  
 RL Microbiology 144:479-492(1998).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP  
 RC STRAIN=HB27;  
 RA Sanchez R., Roovers M., Glansdorff N.;  
 RT "Organisation of arginine biosynthetic genes in *Thermus thermophilus*";  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: N(2)-Acetyl-L-ornithine + L-glutamate - L-  
 CC ornithine + N-acetyl-L-glutamate.  
 CC -1- PATHWAY: Arginine biosynthesis; fifth step.  
 CC -1- SUBUNIT: Heterotetramer of two alpha and two beta chains (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).  
 CC -1- MISCELLANEOUS: Some bacteria possess a monofunctional argJ, i.e., capable of catalyzing only the fifth step of the arginine biosynthetic pathway.  
 CC -1- SIMILARITY: Belongs to the argJ family.

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 CC  
 DR EMBL; Y10525; CRA71551\_1.; DR EMBL; Y1B53; CRA77143\_1.; DR HAMAP; MF\_01106; ; 1.  
 DR InterPro; IPR002813; ArgJ.  
 DR Pfam; PF01960; ArgJ; 1.  
 DR ProDom; PD004133; ArgJ; 1.  
 DR TIGR4MS; TIGR0120; ArgJ; 1.  
 DR Arginine biosynthesis; Transferase; Acyltransferase.  
 FT CHAIN 1 175 GLUTAMATE N-ACETYLTRANSFERASE ALPHA CHAIN  
 FT CHAIN 1 175 GLUTAMATE N-ACETYLTRANSFERASE BETA CHAIN  
 FT SITE 188 189 CLEAVAGE (NONHYDROLYTIC) (BY SIMILARITY).  
 FT SITE 381 AA; 40318 MW; 1605C5B17B7B05A8 CRC64;  
 SQ SEQUENCE 381 AA; 40318 Length 362;

Query Match 36.8%; Score 7; DB 1; Length 381;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 365 ||||||| ARRAAR 371

Qy 4 ARRAAR 10  
 Db 274 ARRAAR 280

RESULT 8

ID SUC2\_STRCO STANDARD; PRT; 383 AA.

AC 087840; DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Succinyl-CoA synthetase beta chain 2 (EC 6.2.1.5) (SCS-beta 2).  
 GN SUC2 OR SC0585 OR SCSA6\_06.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetes;  
 OC Streptomyceae; Streptomyctaceae; Streptomyces.  
 OX NCBI\_TAXID=1902;

[1] RN SEQUENCE FROM N.A.  
 RZ STRAINA3(2) / M145;  
 RX MEDLINE=213996410; PubMed=12000953;-  
 RA Bentley S.D., Chater K.F., Cereno-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Taylor S.,  
 RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RR Complete genome sequence of the model actinomycete Streptomyces  
 RR coelicolor A3(2);  
 RL Nature 417:141-147 (2002).

-|- CATALYTIC ACTIVITY: ATP + succinate + CoA = ADP + succinyl-CoA +  
 CC phosphate.  
 CC -|- PATHWAY: Tricarboxylic acid cycle.  
 CC -|- SUBUNIT: Composed of an alpha chain and a beta chain (By  
 CC similarity).  
 CC -|- SIMILARITY: Belongs to the succinate/malate CoA ligase beta  
 CC subunit family.

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 CC or send an email to license@isb-sib.ch).

CC DR EMBL; AL939128; CAA19778.1; -.  
 CC PIR; T35773; T35773.  
 CC HSSP; P07450; 1SCU.  
 CC DR InterPro; IPR003135; ATP-grasp.  
 CC DR InterPro; IPR005809; CoA\_11g\_beta.  
 CC DR Pfam; PF002222; ATP-grasp; 1.  
 CC DR Pfam; PF00549; Ligase-CoA; 1.  
 CC DR TIGRFAMS; TIGR0106; succinobeta; 1.  
 CC DR PROSITE; PS01217; SUCCINYL\_COALIG\_3; 1.  
 CC KW Ligase; Tricarboxylic acid cycle; Complete proteome.  
 CC SEQUENCE 383 AA; 40161 MW; 5A3D05C0FB1DD03 CRC64;

Query Match 36.8%; Score 7; DB 1; Length 383;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Ft CHAIN 173 387  
 Kw SEQUENCE 387 AA; 41840 MW; ED311EC1F47D56DD CRC64;

PROTEIN ARG1 ALPHA CHAIN (BY SIMILARITY).  
 ARGinine BIOSYNTHESIS BIFUNCTIONAL PROTEIN ARG1 BETA CHAIN (BY SIMILARITY).

Qy 3 ARRAAR 9

Query Match Score 7; DB 1; Length 387;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ARRAARA 10  
 |||||  
 Db 276 ARRAARA 282

RESULT 10  
 FXD3\_CHICK STANDARD; PRT; 394 AA.  
 ID FXD3\_CHICK  
 AC P79772;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE helix box protein D3 (HNF3/FH transcription factor, genesis) (Winged  
 GN FOXD3.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 Gallus.  
 NCBI\_NaxID:9031;  
 RN [1]

SEQUENCE FROM N.A.  
 TISSUE-EMBRYO;  
 MEDLINE=97141794; PubMed=8088052;  
 RA Freyaldenhoven B.S., Freyaldenhoven M.P., Iacoboni J.S., Vogt P.K.;  
 RT "Aberrant cell growth induced by avian winged helix proteins.";  
 RL Cancer Res. 57:123-129(1997).

-I- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.

-I- SUBCELLULAR LOCATION: NUCLEAR.

CC -I- SIMILARITY: Contains 1 fork head domain.

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CC -I- PROBABLE TRANSCRIPTION FACTOR.

CC -I- SUBCELLULAR LOCATION: NUCLEAR.

CC -I- SIMILARITY: Contains 1 fork head domain.

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CC -I- PROBABLE TRANSCRIPTION FACTOR.

CC -I- SUBCELLULAR LOCATION: NUCLEAR.

CC -I- SIMILARITY: Contains 1 fork head domain.

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CC -I- PROBABLE TRANSCRIPTION FACTOR.

CC -I- SUBCELLULAR LOCATION: NUCLEAR.

CC -I- SIMILARITY: Contains 1 fork head domain.

DR U37274; AAC60066.1;  
 DR HSSP; Q63245; 2HFF.  
 DR TRANSFAC; T02495;  
 DR InterPro; IPR001766; TF\_Fork\_head.  
 DR PFAM; PF00250; Fork\_head\_1.  
 DR PRINTS; PR00053; FORKHEAD.  
 DR PRODOM; PD000425; TF\_Fork\_head; 1.  
 DR SMART; SM00339; FH\_1.  
 DR PROSITE; PS00657; FORK\_HEAD\_1.  
 DR PROSITE; PS00658; FORK\_HEAD\_2; 1.  
 DR PROSITE; PS50039; FORK\_HEAD\_3; 1.  
 KW DOMAIN 67 70 POLY-ALA.  
 FT DOMAIN 80 91 POLY-GLY.  
 FT DOMAIN 100 106 POLY-ALA.  
 FT DNA\_BIND 117 211 FORK\_HEAD.  
 SQ SEQUENCE 394 AA; 40995 MW; 324A4B36B9E31899 CRC64;

Query Match Score 7; DB 1; Length 394;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RAARRAA 8  
 |||||  
 Db 62 RAARRAA 68

RESULT 12  
 CESS\_HUMAN STANDARD; PRT; 423 AA.  
 ID CESS\_HUMAN  
 AC Q9BXW7; Q9BXW8; Q9NWA8; Q9NX41;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Cat eye syndrome critical region protein 5 precursor.  
 GN CESCR5  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID:9606;  
 RN [1]

SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 MEDLINE=21275466; PubMed=11381032;  
 Pootz T.K., Brinkman-Mills P., Banting G.S., Maier S.A., Riazi M.A.,  
 Bridgland L.J., Hu S., Birren B., Minoshima S., Shimizu N., Pan H.,  
 Nguyen T., Fang F., Fu Y., Ray L., Wu H., Shauli S., Yao Z.,  
 Chen F., Hoan A., Hu P., Wang Q., Loh P., Qi S., Roe B.A.,  
 McBerndt H.E.;  
 "Analysis of the cat eye syndrome critical region in humans and the  
 region of conserved synteny in mice: a search for candidate genes at  
 or near the human chromosome 22 pericentromere.";  
*Genome Res.* 11:1053-1070(2001);  
 [2].  
 SEQUENCE FROM N.A. (ISOFORM 2).  
 TISSUE=Embryo, and Gastric carcinoma;  
 Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
 Nagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
 Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
 Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.,  
 Ninomiya K., Iwayangki T.;  
 "NEDO human cDNA sequencing project."  
 Submitted (FEB-2000) to the EMBL/GenBank/DDJB databases.  
 [3].  
 SEQUENCE FROM N.A. (ISOFORM 2).  
 TISSUE=Lymph;  
 PubMed=112477932;  
 RA Straubinger R.L., Feingold E.A., Grouse L.H., Dervic J.G.,  
 RA Klaunser R.D., Collins F.S., Wagner L., Schueler G.D.,  
 RA Altschul S.F., Zeberg B., Bustot K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Heilton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grumwood J., Schmitz J., Myers R.M.,  
 RA Burrows Y.S.N., Krawinski M.I., Stalska U., Smallius D.E.,  
 RA Schnier A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 -1 ALTERNATIVE PRODUCTS:  
 Event-Alternative splicing; Named isoforms=2;  
 Name=2;  
 IsoId=Q9BXW7-1; Sequence=Displayed;

CC IsoId=Q9BXW7-2; Sequence=vSP\_003840;  
 CC -1 TISSUE SPECIFICITY: Widely expressed.  
 CC -1 MISCELLANEOUS: Candidate gene for the Cat Eye Syndrome (CES), a  
 development disorder associated with the duplication of a 2 Mb  
 region of 22q11.2. Duplication usually takes in the form of a  
 supernumerary bisatellited isodicentric chromosome, resulting in  
 four copies of the region (represented an inv dup(22)(q11)). CES is  
 characterized clinically by the combination of coloboma of the  
 iris and anal atresia with fistula, downslanting palpebral  
 fissures, preauricular tags and/or pits, frequent occurrence of  
 heart and renal malformations, and normal or near-normal mental  
 development.

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 or send an email to license@isb-sib.ch).

DR EMBL; AF273271; AAK19152; 1;  
 DR EMBL; AF273270; AAK19151; 1;  
 DR EMBL; AK001034; BAA91475; 1;  
 DR EMBL; AK000461; BAA91180; 1;  
 DR EMBL; BC042540; AAH2540; 1;  
 DR Geneva; HGNC:18A3; CBER5;  
 DR InterPro; IPR006353; HAD\_CECRS;  
 DR InterPro; IPR006357; HAD\_SF-IIA;  
 DR TIGRFAMS; TIGR01456; CECRS; 1;  
 DR TIGRFAMS; TIGR01460; HAD\_SF-IIA; 1;  
 KW POTENTIAL: 5;  
 FT SIGNAL; Alternative splicing. 23;  
 FT CHAIN 24 423 CAT EYE SYNDROME CRITICAL REGION PROTEIN  
 MAAWGCGVAALGARGLCWRAAFAAGIQLGPRARRCYANGPA  
 >NM174815FS (in isoform 1).  
 /FTID=vSP\_003840.  
 D -> N (IN REF. 2; BAA91180);  
 V -> F (IN REF. 2; BAA91475);  
 E -> G (IN REF. 2; BAA91475);  
 SQ 423 AA: 46321 MW: C4DD208ABBB8CCE CRC64;

Query Match 36.8%; Score 7; DB 1; Length 423;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 RAARARA 12  
 ||||| |  
 Db 19 RAARARA 25

RESULT 13  
 Y486 MYCLE STANDARD; PRT; 428 AA.  
 ID Y486\_MYCLE  
 AC P54138; Q9CB50;  
 DT 01-09-1996 (Rel. 34, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-JUL-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical protein ML2443;  
 GN ML2443 OR U2158F OR B2168\_C2\_201.  
 OS Mycobacterium leprae.  
 OC Bacteria; Actinobacteria; Actinomycetales;  
 CORNEBACTERIAE; Mycobacteriaceae; Mycobacterium.  
 NCBI\_TaxID=1769;  
 RN [1] RP SEQUENCE FROM N.A.  
 RA Smith D.R., Robison K.;  
 RL Submitted (MAR-1994) to the EMBL/GenBank/DDJB databases.  
 RN [2] RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-TN;  
 RX MEDLINE=21128712; PubMed=11234002;  
 RA Cole S.T., Eigenthaler J., Parkhill J., James K.D., Thomson N.R.,  
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,  
 RA Mundall K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,  
 RA Hollroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,  
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,  
 RA Rutledge S., Seeger K., Simon S., Skelton J., Squares R.,  
 RA Stevens K., Whitehead S., Woodward J.R.,  
 RA Barrell B.G.;  
 RT "Massive gene decay in the leprosy bacillus.";  
 RL Nature 409:1007-1011(2001).  
 CC -1 SIMILARITY: TO M TUBERCULOSIS RV0486.

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DR EMBL; U00018; AAA17228.1; ALT\_INIT.  
 EMBL; AL583925; CAC31960.1; -.  
 DR PR: H87214; H87214.  
 Leproma; ML2443; -.  
 DR InterPro; IPR001296; Glyco\_trans\_1.  
 DR Pfam; PF0054; Glycos\_transf\_1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 428 AA; 45291 MW; Al4FF0187B3587C CRC64;  
 [1] Query Match 36.8%; Score 7; DB 1; Length 428;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 RRAARRAA 11  
 Db 204 RRAARRAA 210

RESULT 14  
 VGLX\_HSVBS STANDARD; PRT; 444 AA.  
 ID VGLX\_HSVBS  
 AC Q08103;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 Glycoprotein GX precursor.  
 DE Bovine herpesvirus type 1.2 (strain ST).  
 OS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Varicellovirus.  
 OX NCBI\_TaxID=45407;  
 RN

RP SEQUENCE FROM N.A.  
 RX MEDLINE=94167875; PubMed=8122370;  
 RA Leung-Tack P.; Audonnet J.-F.; Riviere M.;  
 RT The complete DNA sequence and the genetic organization of the short  
 RT unique region (US) of the bovine herpesvirus type 1 (ST strain).  
 RL Virology 199:409-421(1994).

CC SEQUENCE FROM N.A.  
 DR EMBL; 223058; CAA80603.1; -.  
 DR PR: S35783; S35783.  
 DR InterPro; IPR00333; Herpes\_gG.  
 DR Pfam; PF02400; Herpes\_gG.  
 KW Glycoprotein; Transmembrane; Signal.  
 FT SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 444 GLYCOPROTEIN\_GX.  
 FT TRANSMEM 390 414 POTENTIAL.  
 FT CARBOHYD 117 117 N-LINKED (GLCNAC, . .) (POTENTIAL).  
 FT CARBOHYD 240 335 N-LINKED (GLCNAC, . .) (POTENTIAL).  
 FT CARBOHYD 335 444 AA; 46708 MW; 0145942A35B05CB CRC64;  
 SQ SEQUENCE [REDACTED]

Query Match 36.8%; Score 7; DB 1; Length 444;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 ARRARA 17  
 Db 422 ARRARA 428

RESULT 15  
 TRME\_XANAC STANDARD; PRT; 448 AA.  
 AC Q8PERH; 143 ARRARA 149

DR SEQUENCE FROM N.A.  
 RC STRAIN=306 / ATCC 13902 / XV 101;  
 RX MEDLINE=22022145; PubMed=12024217;  
 RA da Silva A.C.R.; Ferro J.A.; Reinach F.C.; Farah C.S.; Furlan L.R.';  
 RA Quaggio R.B.; Monteiro-Vitorello C.B.; Van Sluys M.A.; Almeida N.F.,  
 RA do Amaral A.M.; Bertolini M.C.; Camargo L.E.A.';  
 RA Camarote G.; Cannavaro F.; Cardozo J.; Chambargo F.; Caprina L.P.,  
 RA Cicarelli R.M.B.; Coutinho L.L.; Corsino-Santos J.R.; El-Dorry H.,  
 RA Faria J.B.; Ferreira A.J.S.; Ferreira R.C.C.; Ferro M.I.T.,  
 RA Formighieri E.F.; Franco M.C.; Greggio C.C.; Gruber A./;  
 RA Katsuyama A.M.; Kishi L.T.; Leite R.P.; Lemos E.G.M.; Lemos M.V.F.,  
 RA Locali E.C.; Machado M.A.; Madeira A.M.B.N.; Martinez J.; Rossi N.M.,  
 RA Martins E.C.; Medeiros J.; Menck C.P.M.; Miyaki C.Y.; Moon D.H.,  
 RA Moreira L.M.; Novo M.T.M.; Okura V.K.; Oliveira M.C.; Oliveira V.R.,  
 RA Pereira H.A.; Rossi A.; Sena J.A.D.; Silva C.; de Souza R.F.,  
 RA Spinola L.A.P.; Takita M.A.; Tamura R.E.; Teixeira E.C.; Tezza R.I.D.,  
 RA Trindade dos Santos M.; Truffi D.; Tsai S.M.; White F.F.,  
 RA Setubal J.C.; Kitajima J.P.;  
 PRT "Comparison of the genomes of two Xanthomonas pathogens with differing  
 host specificities.";  
 RL Nature 417:459-463 (2002).

CC FUNCTION: Exhibits a very high intrinsic GTPase hydrolysis rate.  
 CC Involved in the biosynthesis of the hypermodified nucleoside 5'-  
 methylaminomethyl-1,2-thiouridine, which is found in the wobble  
 CC position of some tRNAs (By similarity).  
 CC -1- SIMILARITY: Belongs to the era/trME family of GTP-binding  
 CC Proteins. TRME subfamily.

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CC DR EMBL; AE012091; AAC32001; -.  
 CC DR HAMAP; MF\_00379; -; 1.  
 CC DR InterPro; IPR005389; GTP-binding\_domain.  
 CC DR TIGRFAMS; TIGR00231; small\_GTP; 1.  
 CC DR InterPro; IPR006073; GTP\_OBG.  
 CC DR InterPro; IPR005225; Small\_GTP.  
 CC DR InterPro; IPR004520; ThdF.  
 CC DR PRINTS; PRO0326; GTP\_OBG.  
 CC DR TIGRFAMS; TIGR00650; MG442; 1.  
 CC DR InterPro; IPR005389; small\_GTP; 1.  
 CC DR TIGRFAMS; TIGR00450; thdF; 1.  
 CC KW tRNA Processing; GTP-binding; Complete proteome.  
 CC FT NP\_BIND 225 232 GTP (POTENTIAL).  
 CC FT NP\_BIND 272 276 GTP (POTENTIAL).  
 CC SQ SEQUENCE 448 AA; 47543 MW; B6B3D163D92E3F4 CRC64;  
 CC Query Match 36.8%; Score 7; DB 1; Length 448;  
 CC Best Local Similarity 100.0%; Pred. No. 25;  
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARRARA 7  
 Db 143 ARRARA 149

Search completed: August 9, 2003, 16:29:50  
 Job time : 11.7714 secs